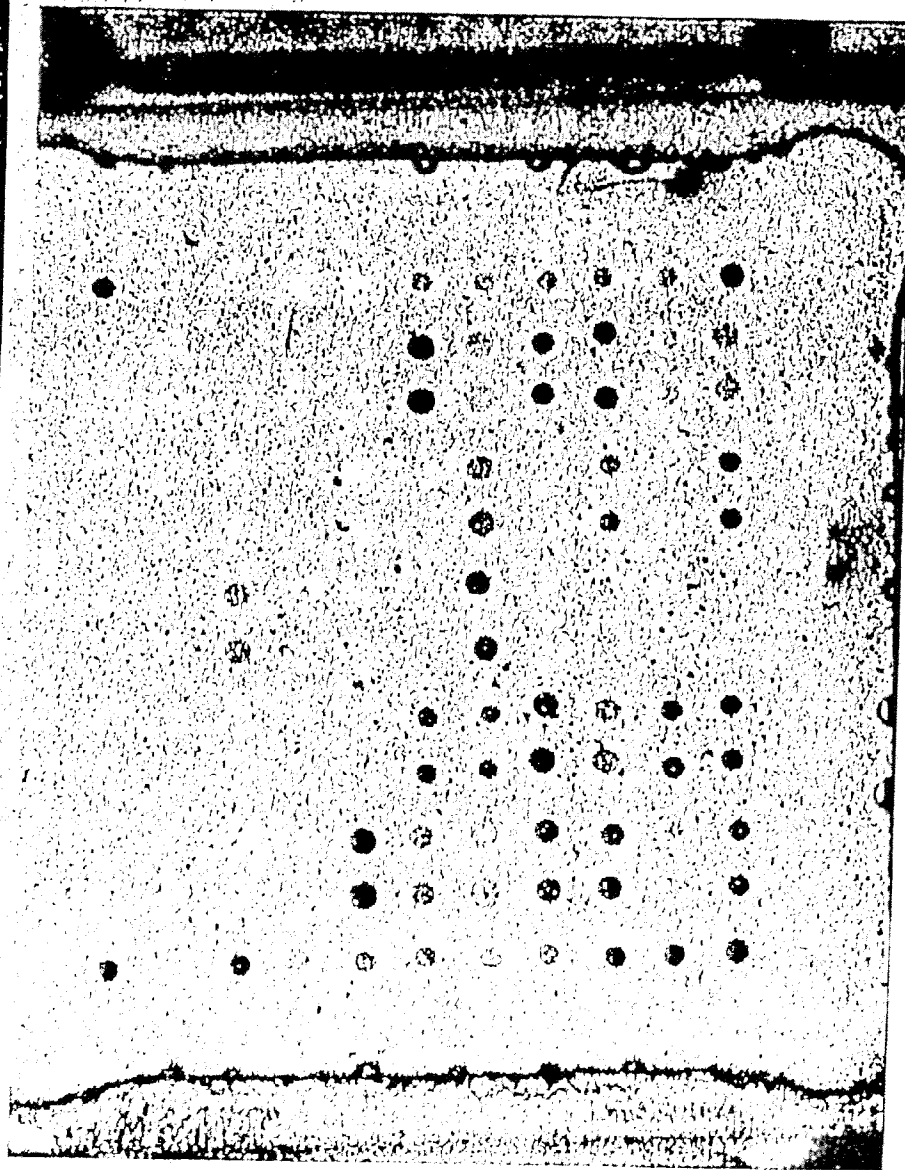


FIGURE 1

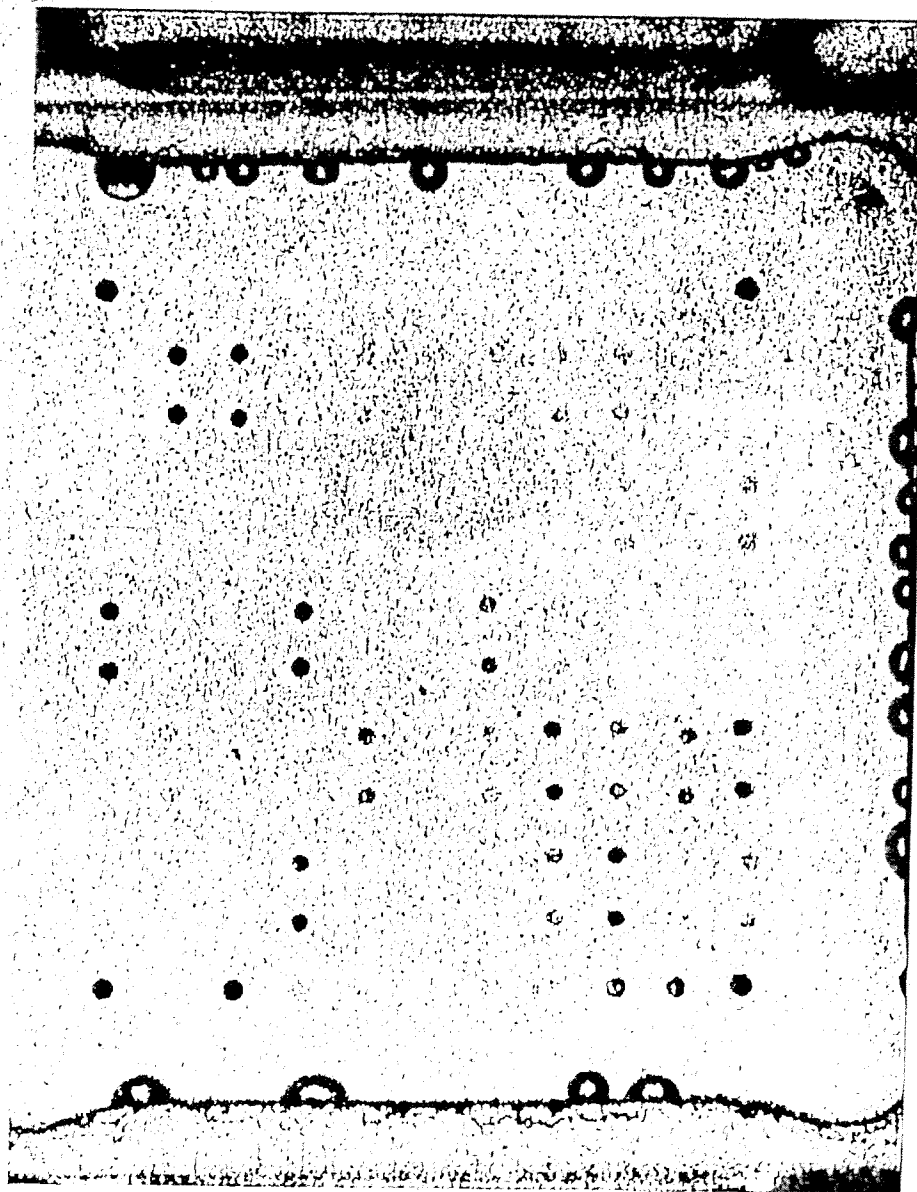
P. aeruginosa AT-Chip



ZW117

FIGURE 2

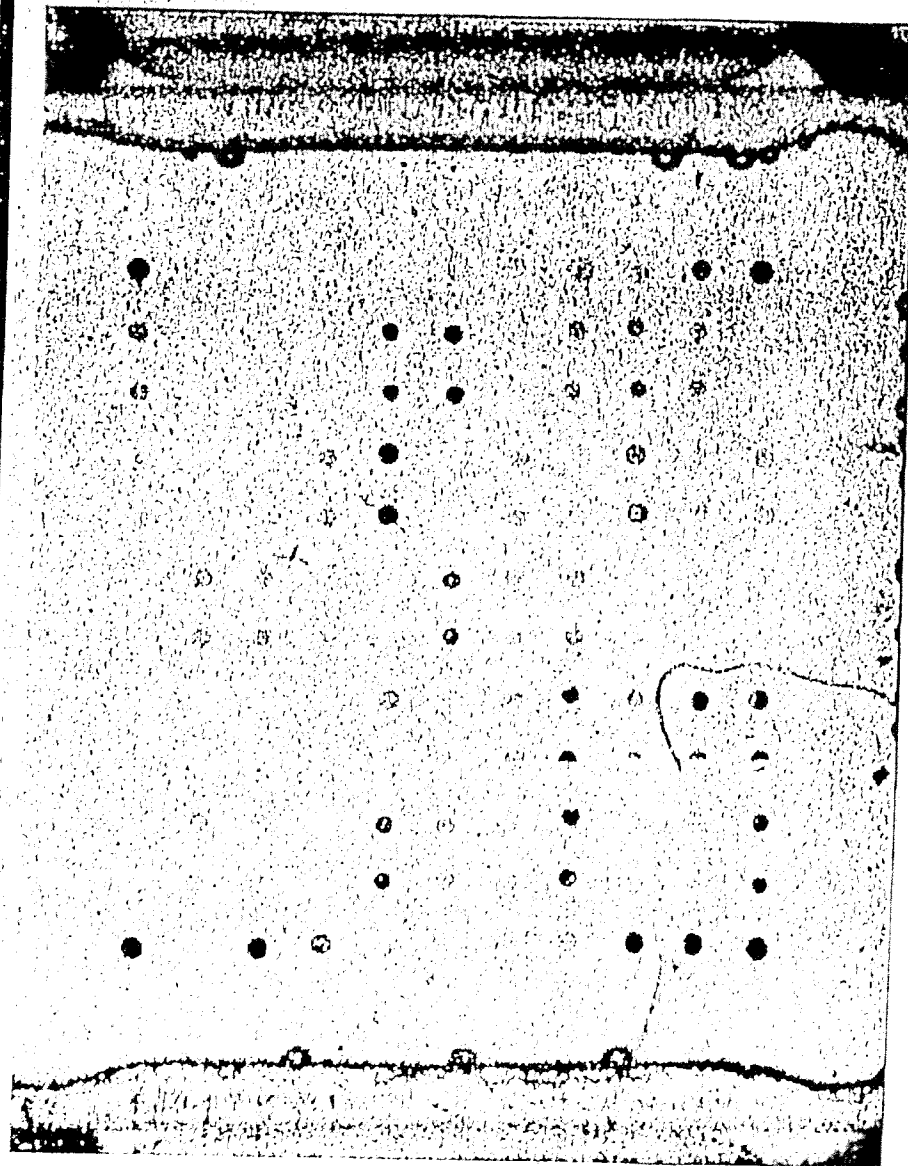
P. aeruginosa AT-Chip



RP17

FIGURE 3

P. aeruginosa AT-Chip



TB

FIGURE 4

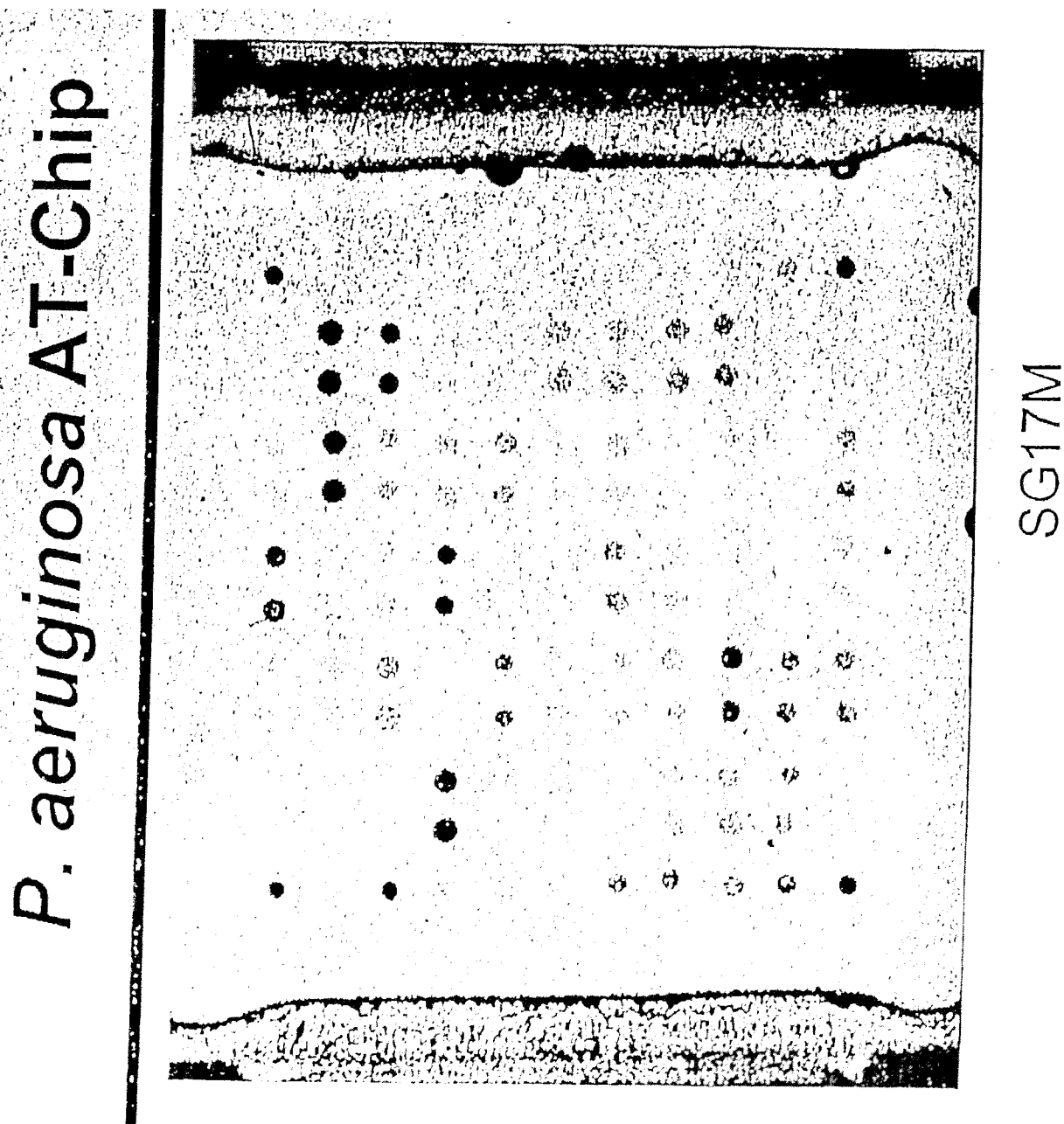
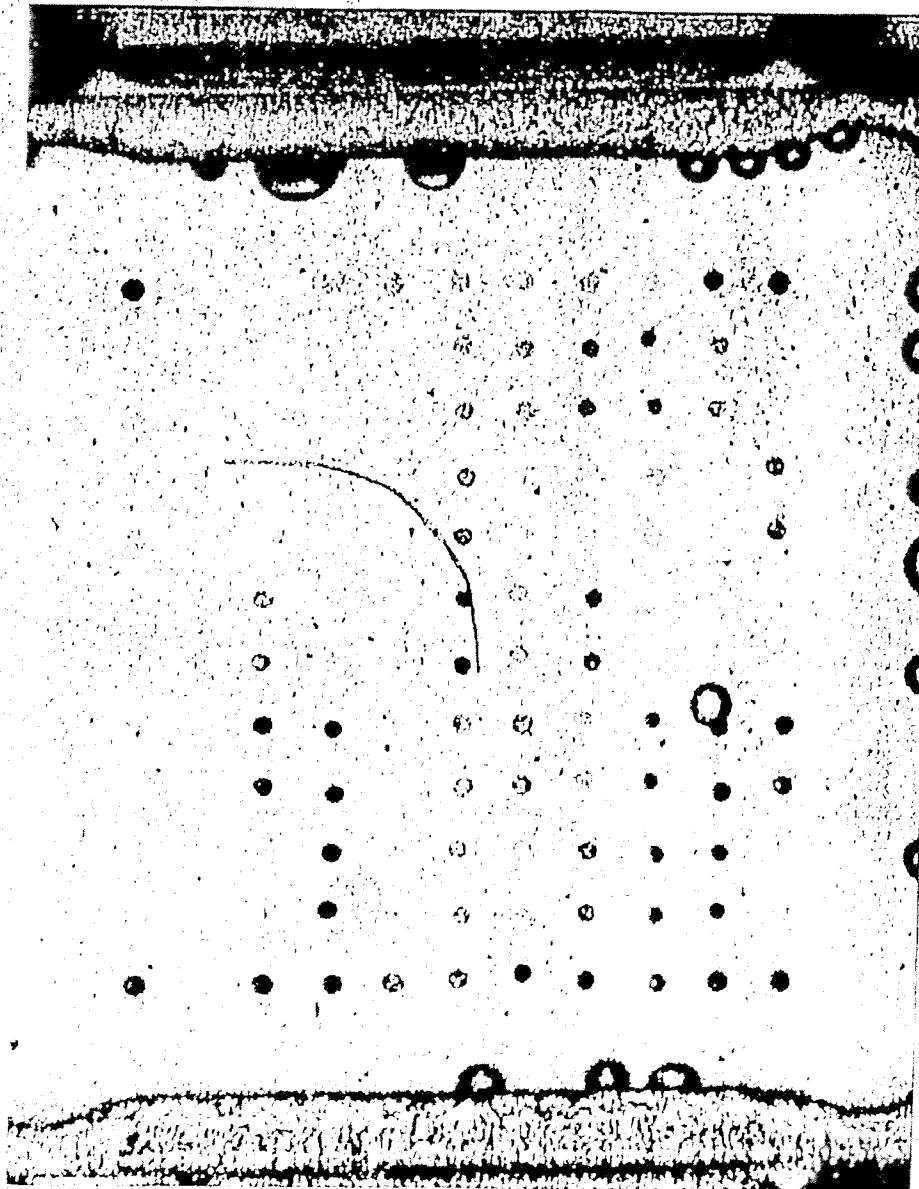


FIGURE 5

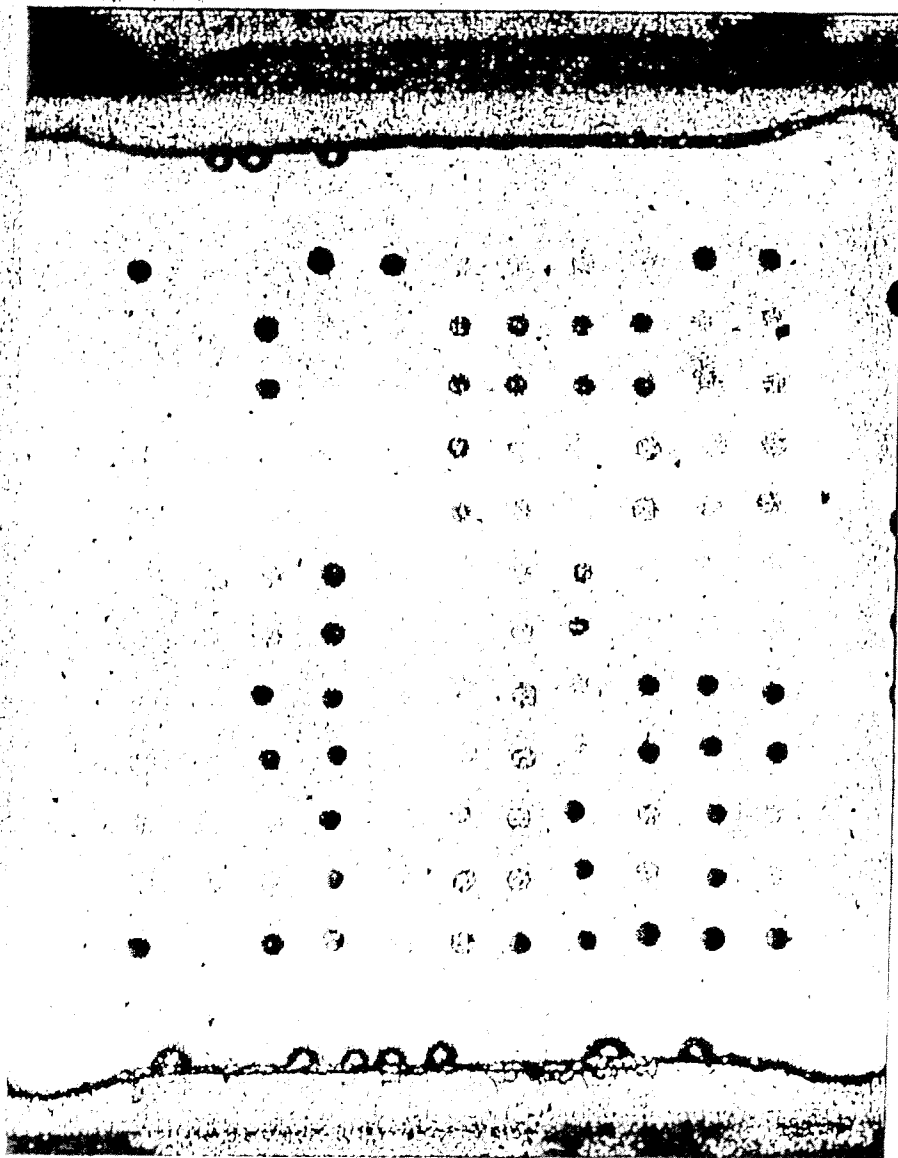
P. aeruginosa AT-Chip



BST85

FIGURE 6

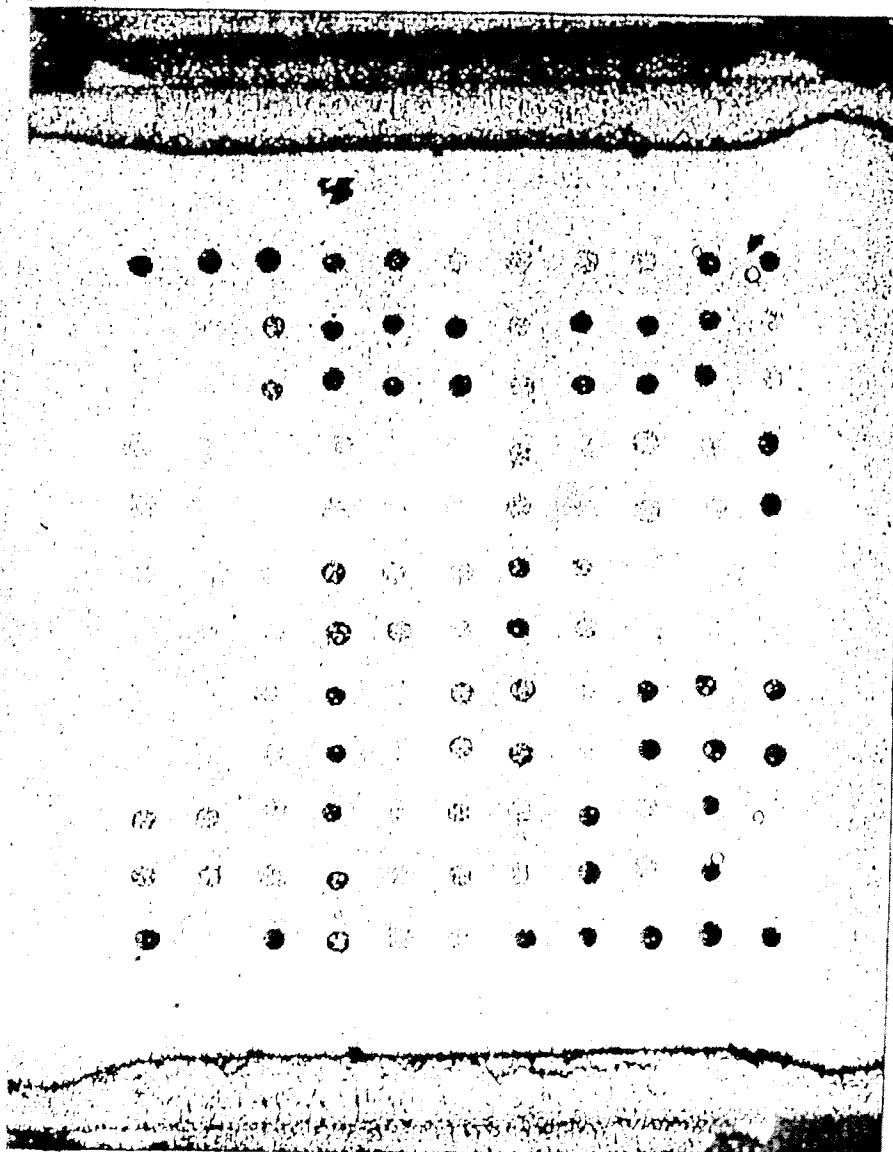
P. aeruginosa AT-Chip



AL5846

FIGURE 7

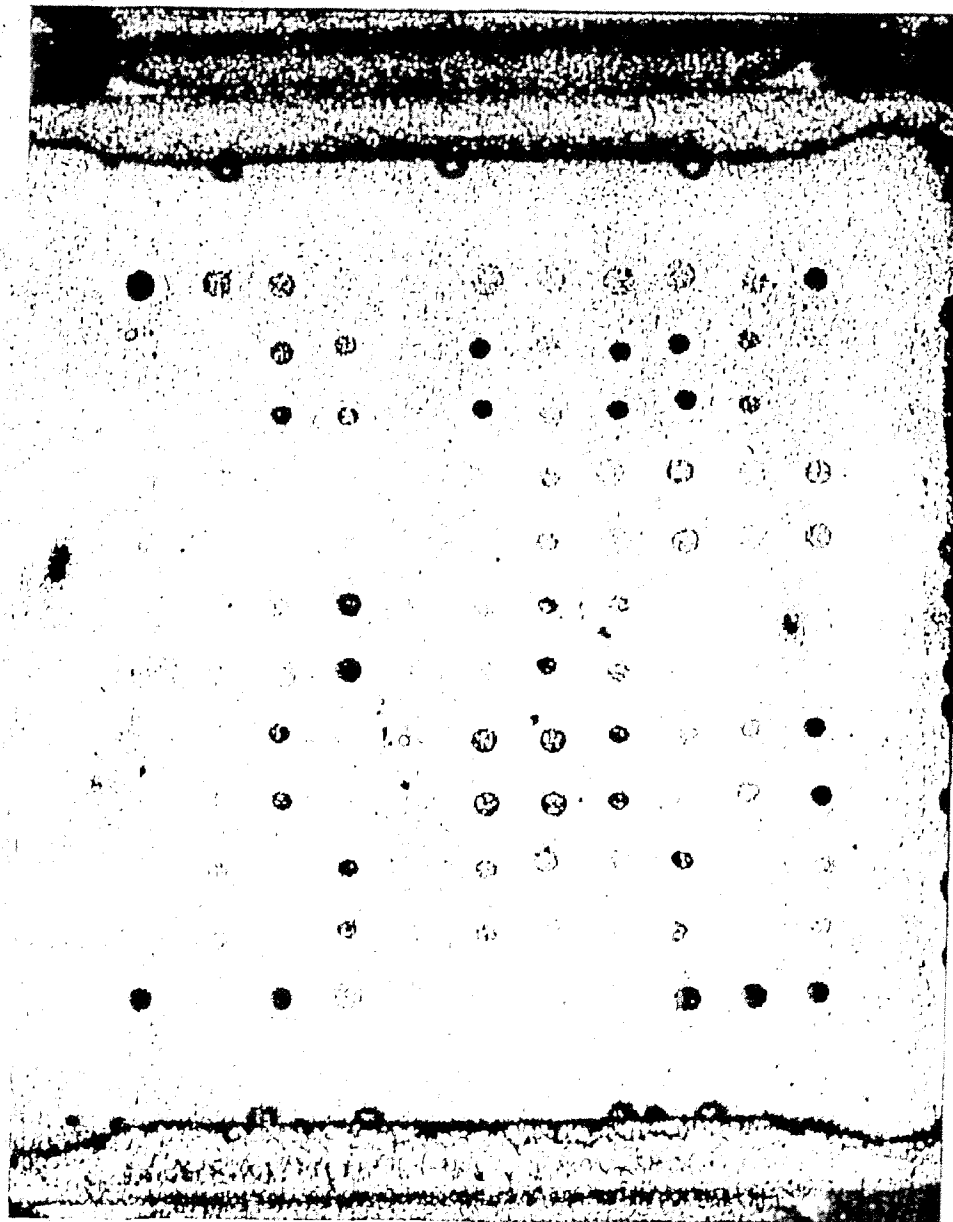
P. aeruginosa AT-Chip



PT12

FIGURE 8

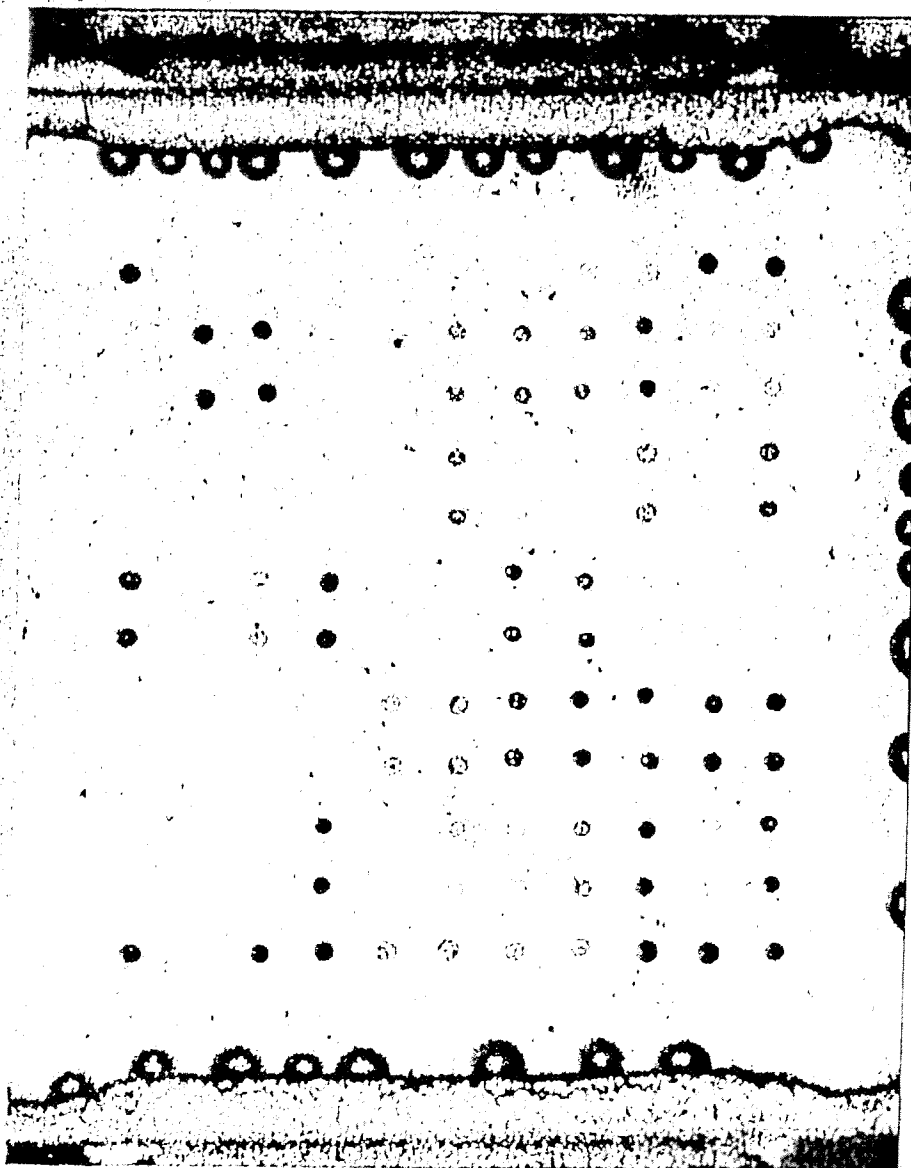
P. aeruginosa AT-Chip



PT20

FIGURE 9

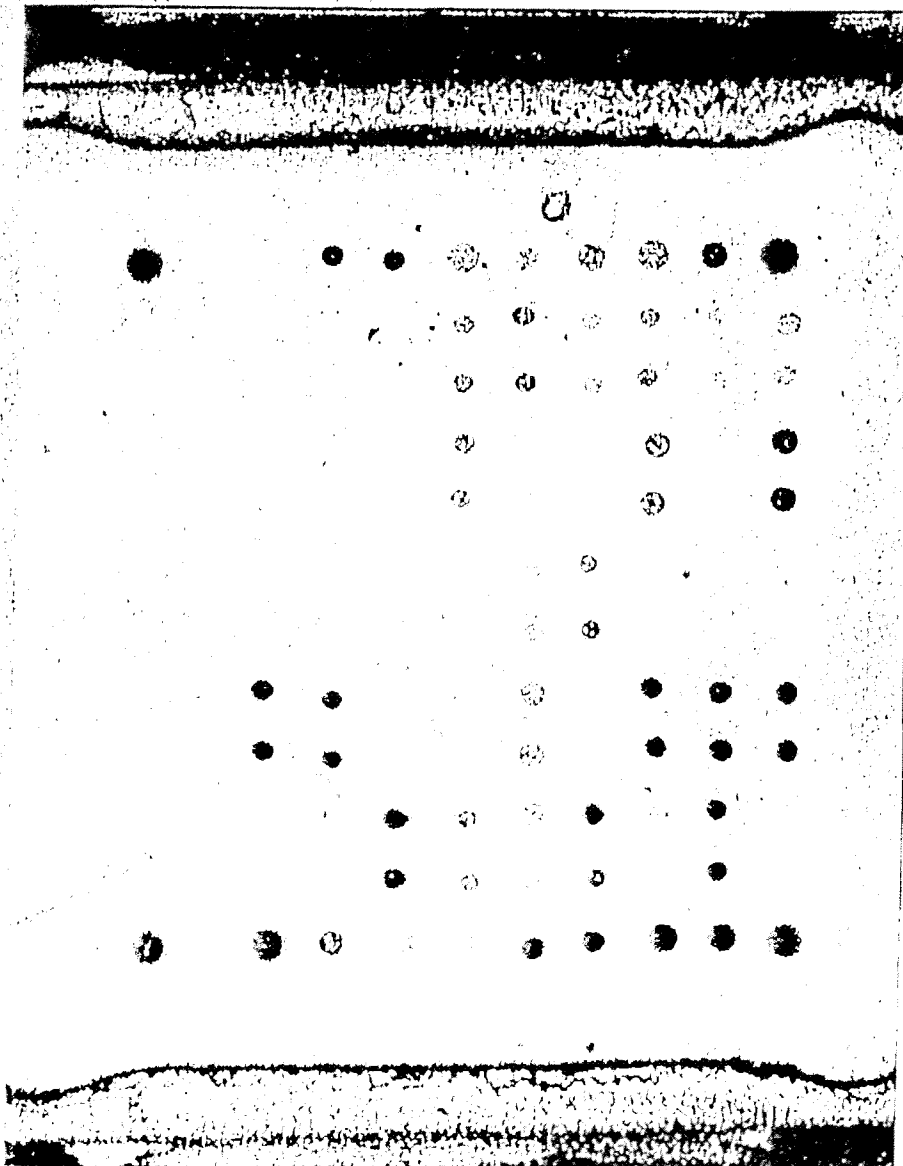
P. aeruginosa AT-Chip



ZW79

FIGURE 10

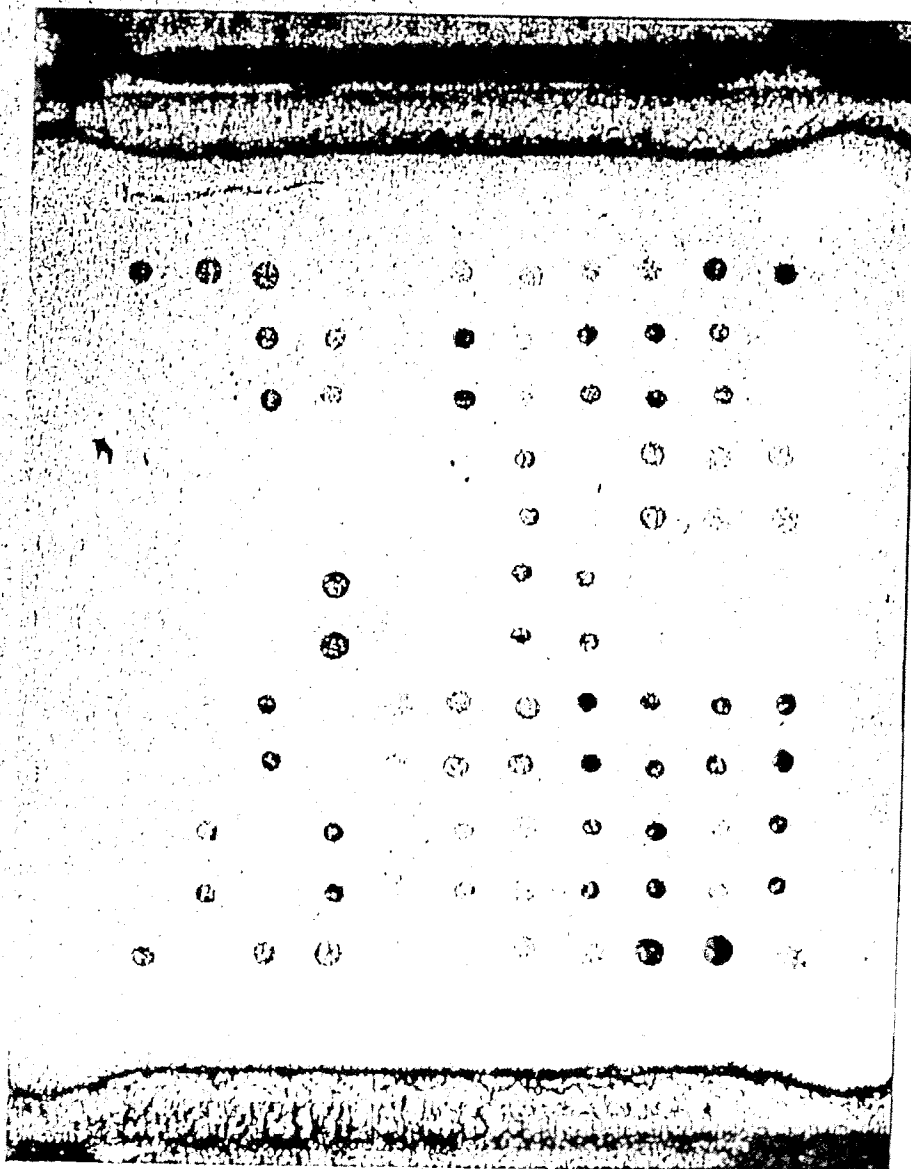
P. aeruginosa AT-Chip



ZW85

FIGURE 11

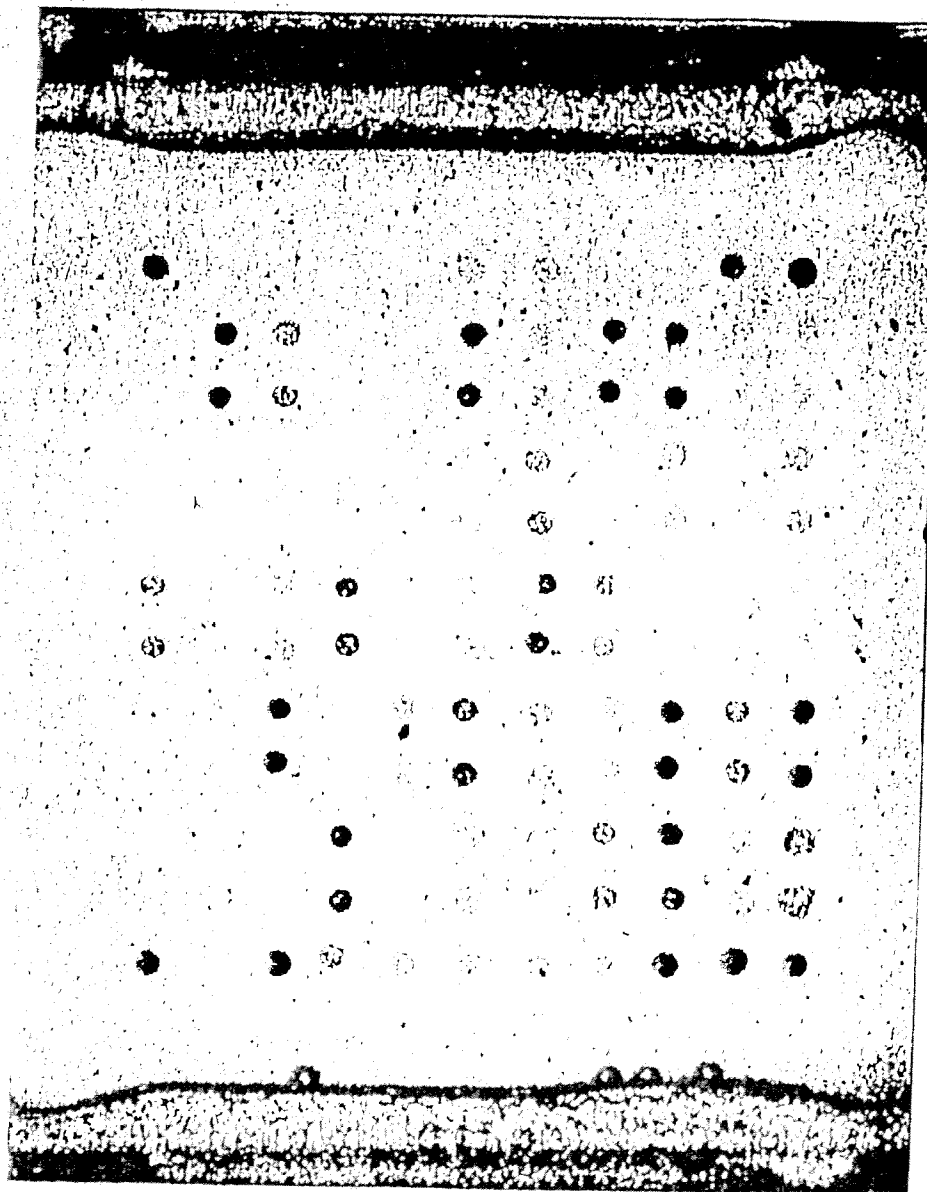
P. aeruginosa AT-Chip



2813A

FIGURE 12

P. aeruginosa AT-Chip



KB1-85

FIGURE 13

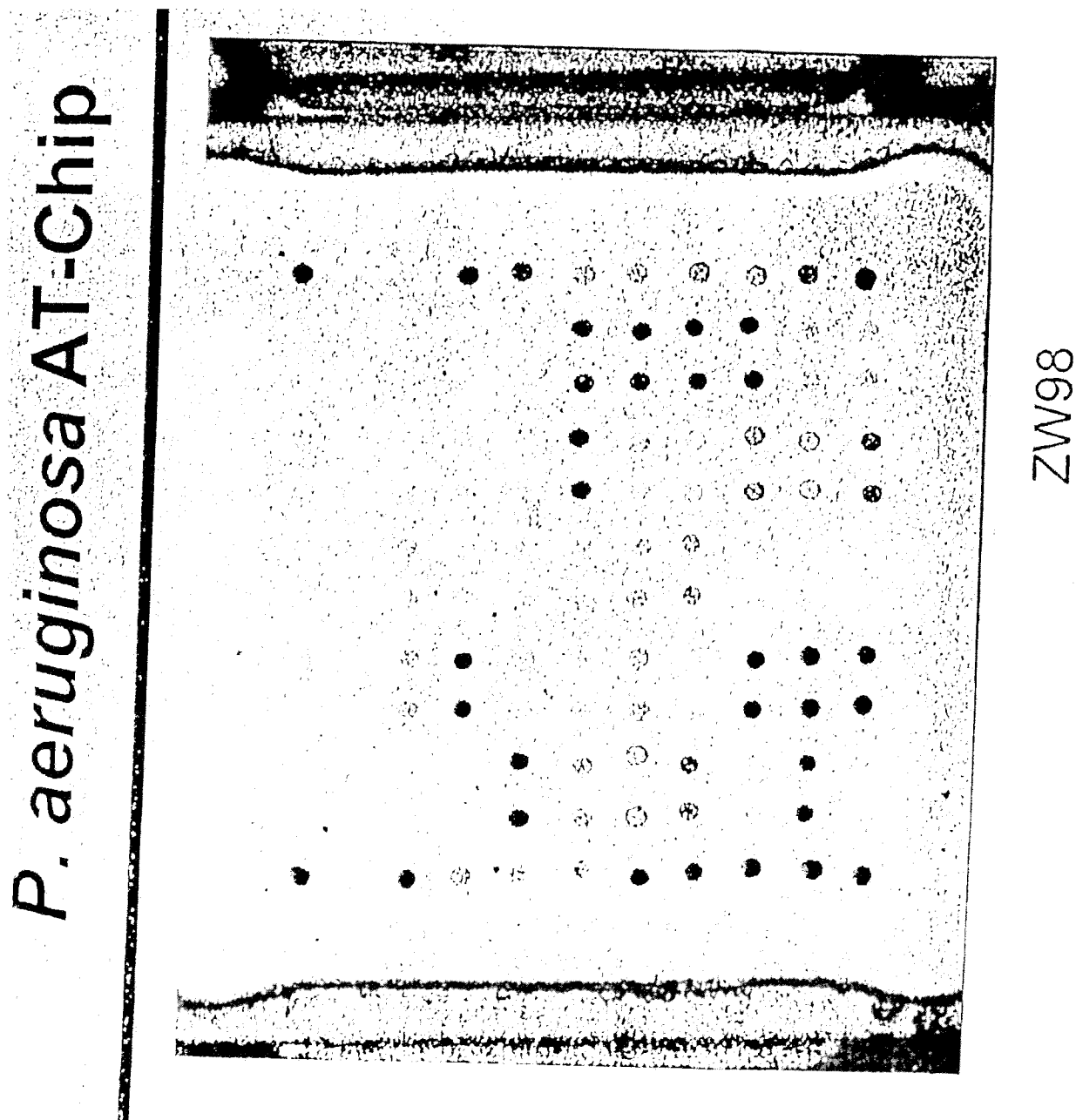
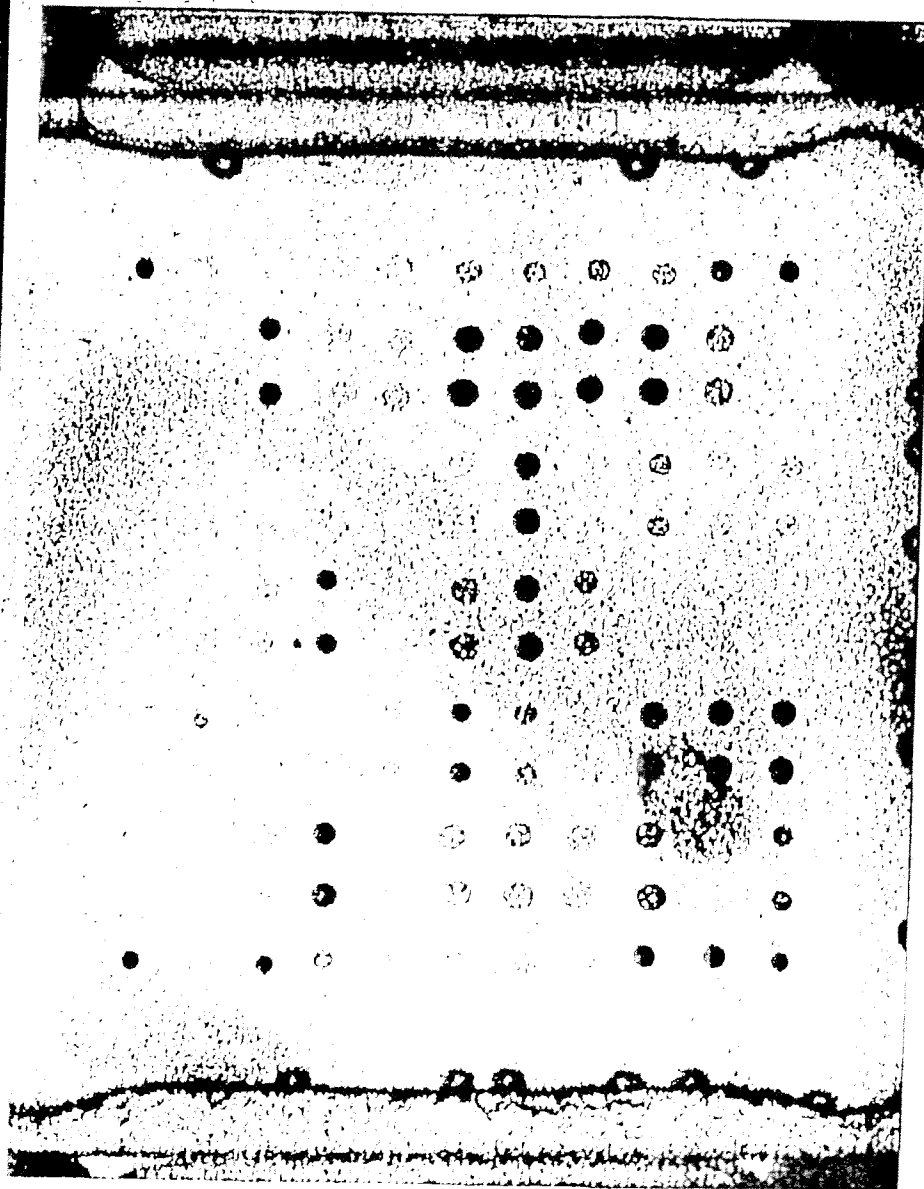


FIGURE 14

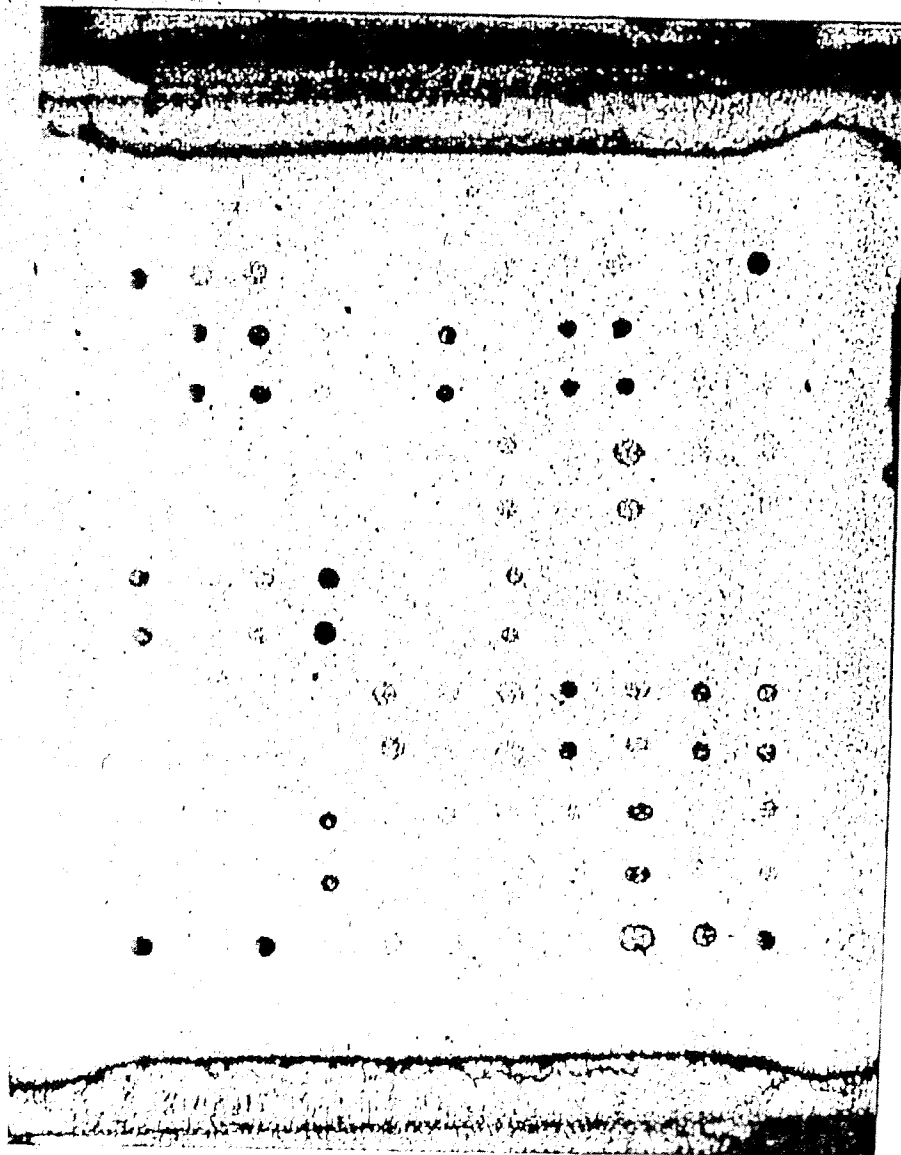
P. aeruginosa AT-Chip



641HD

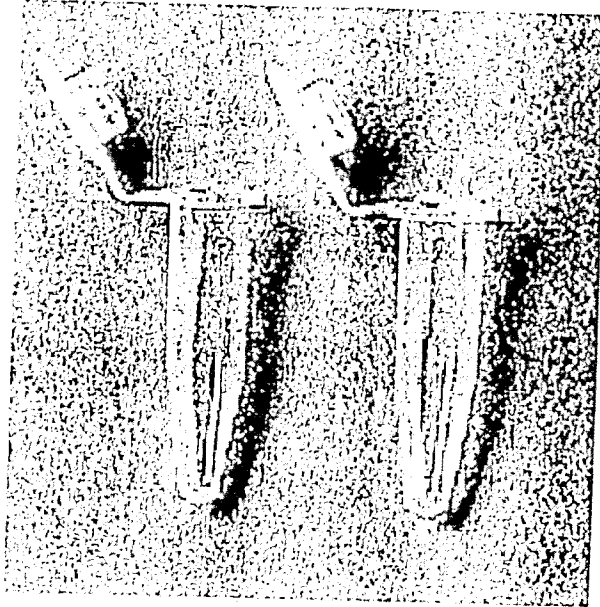
FIGURE 15

P. aeruginosa AT-Chip



ATCC15522

FIGURE 16



REPLACEMENT SHEET

Atty Docket: 15111.0087

FIGURE 17A

47-1/23
ACGCGGATGTCCTGGATTGG

47-1/39
CTGAAGAAGGGGCGCTACGCG

47-2/22
GCGTACCGGGCAAGGTGATAG

47-2/52
CTCGGTGAAACATCGGGAGGG

C45/18
TCATCCAGCAAGCCATTGCGC

C45/60a
GGAGTCGCTTTCCGCCATCG

C45/60b
TGGAGTCGCTTTCCGCCATCG

C46/15
AAGGGCGTTTCACGCTGACGC

C46/22
ATCCGGAAGGGCGTTTCACG

C46/88
TCCACACCTCAGACTTCGGCG

C47-1/43
TATTGACGACCTACCGCGCGC

C47-2/56a
GCAACTGATGTTGCCCCAGC

C47-2/56b
CGCAACTGATGTTGCCCCAGC

C47-2/59
ACACGCAACTGATGTTGCCCC

CIS-4/36
TGTCCCGGCTCAGTTCAACG

CIS-4/50
AACACCTTGGCGTTTGTCCC

CIS-4/51
GCAACACCTTGGCGTTTGTCC

CIS-5/4
TCAAGCTCGTTGTGGACCGC

CIS-5/48
GTTACGACGGCGTGCTGTCCG

CSP-1/39a
ACGCAACGTATTGCGCGACCC

CSP-1/39b
CGCAACGTATTGCGCGACCC

FIGURE 17B

fliAT/28
AGCTGATGGTATCGCCGTCGC

fliAT/72
CTAGTGATCGCACCGGAGCC

oriC/20
AGCCTCGACACCGGTTCTCG

oriC/54
TCGTTTCATCCCCAGGCTTCG

oriC/59
ACCATCTCGTTTCATCCCCAGG

oprL/53
TTCTGAGCCCAGGACTGCTCG

oprL/65
TCGACGCGACGGTTCTGAGCC

fliCb/36
TGACGTTCTCGCCGGTAGCG

fliCb/65
CAGTAGCGGTACCGGTCTGCG

fliCb/66
CAGTAGCGGTACCGGTCTGC

alkAG/27
TTCTCGCCGGCATAGTAGGC

alkGA/32

alkGA/51
CGAGGACGAGGCATCTCCGG

citAG/4
GCAGGTAGCAGGTTTCCAGG

citAG/46
AACTGTTTCCTTCTGCGCGGCG

citGC/8
TGATCGGCTTGGTCTCGCAGG

citGC/11
GCTGATCGGCTTGGTCTCGC

citGC/75
GAGGCGTTCTGCTCGTGGTCG

oprI/12
TTTTTCCAGCATGCGCAGGG

oprI/17
GCTGGCTTTTTCCAGCATGCG

oprI/22
TTGCGGCTGGCTTTTTCCAGC

REPLACEMENT SHEET

Atty Docket: 15111.0087

FIGURE 17C

am7CA/1
TTGGGATAGTTGCGGTTGGC

am7CA/27
CGTAGGCGATCTTCACCCGC

am7CA/29
TGGCGTAGGCGATCTTCACCC

am3CT/21
GGCGAGATAGCCGAACAGGC

am3CT/22
GCGGCGAGATAGCCGAACAGG

am3CT/69
CACTTGCTGCTCCATGAGCC

am2CT/35
GAGGTCGAGCAGGCTGATGC

am2CT/42
TAGGTCGCGAGGTCGAGCAGG

am2CT/92
GTCCTTCTGCACCGAGTCGG

am1GA/49
CGCATCTTGTCTGGGTCAGG

am1GA/58
TCGTGAGGCGCATCTTGTCC

am45/1
ACGTGAGGTGGGTCTGTTCC

am45/96
GTAGCCTTCGGCATCCAGCG

am6TC/60
TCGGCATTGGGATAGTTGCGG

GI11/15
CCTCCTGTCTCATGCCGATGC

GI11/59
GCATTGCCCACGGAAGGAAGG

GI11/71
GAAGGCATCATGGCATTGCGCC

GI18/62
GTCATGGGGTTTCCCAGAGACC

fliCa/41
GATCGCGATGTCGACGGTGCC

fliCa/42
CGATCGCGATGTCGACGGTGCC

fliCa/46
TGCCGATCGCGATGTCGACG

REPLACEMENT SHEET

Atty Docket: 15111.0087

FIGURE 17D

SG-1/40
GACGAATACCCAGCTGCGTGG

SG-1/43
GCAGACGAATACCCAGCTGCG

SG-4/1
CGCGACGTCGTGACGTCAGC

SG-4/67
ACTTTCGGCTCTTCGGGCTGG

TB46/21
AGGTAGAGACTCGGGGAACC

TB46/45
TCGTTTTCGGTCATGGCCAGG

TB471/22
TTCCGCGACGAACATCCGTGG

TB471/25
CGCTTCGCGACGAACATCCG

TB472/36
GGATCGCTTCCGATAGGGCAGC

TB472/84
AGAGGCATGGGTCTGTACCG

TB473/34
TCTGTCAATCCCCTTGGGG

TB473/41
AGCCCCTTTCTGTCAATCCCC

TB474/36
GGCTTCCTACCGAAGGTCAGG

TB474/41
TGAGGGCTTCCTACCGAAGG

exoS/31
TTCAAGGTCATGGGCAATGCC

exoS/37
AGTCCCTTCAAGGTCATGGGC

exoU/22
GCCGACTGAGCTGTAGCTCGG

exoU/23
GGCCGACTGAGCTGTAGCTCG

exoU/42
ACCAGACTGGTCAATGGTGG

flins/2
CCCGTGTTCCGTAGACCTTGC

pKL11/49a
AGCAGTTACCCACAGCATGG

REPLACEMENT SHEET

Atty Docket: 15111.0087

FIGURE 17E

pKL11/49b
CAGCAGTTACCCACAGCATGG

pKL3/47
CTACACTCCAACCGCTGGTCC

pKL3/50
GACCTACACTCCAACCGCTGG

pKL3/80
TTCCCTTGCTGCCGAGAAGC

pKL7/14
TAATAGGCGAGCCTGCCGTCC

47D7nw1a
TCCACGCCGAGGGACGTGCC

47D7nw1b
GCTCCACGCCGAGGGACGTGCC

C46-nw1a
CGCGGTGCTGGTTGCGCTGC

C46-nw1b
CCAATGCCCAGGGCCAGCGGA

C46-nw1c
CGCTGGCAGTTCCGCTGGCC

ExoSnw1a
CAGGGTCGCCAGCTCGCTCGCC

ExoSnw1b
AGGGTCGCCAGCTCGCTCGC

ExoUnw1a
AGTGATCTGCCGCGGCCCTGCC

ExoUnw1b
GTGATCTGCCGCGGCCCTGC

OrfA-1
GTTCCACAGGCGCTGCGGCGC

OrfA-2
GTTCCACAGGCGCTGCGGCG

OrfA-3
CAAAGCCCCTGGTCGCGCGG

OrfC-1
GCAGCTTTTCCACCGCCGCGCGG

OrfI-1
AAACTGCCCCGCCCCCATCC

OrfI-2
GGAAAACTGCCCCGCCCCC

OrfJ-1
ACGCTCGCAGCGCCTCACGCG

REPLACEMENT SHEET

Atty Docket: 15111.0087

FIGURE 17F

OrfJ-2
GGCCTGGCTGCGAACGCTCGC

REPLACEMENT SHEET

Atty Docket: 15111.0087

FIGURE 18A

no	label	name	5'-3'-sequence	group	length	GC-content [%]	Tm [°C]	spot-ID's
1	Pa-S_056	oriC T-C_wt	GAAGCCCGGCGAATTCGGTGTTC	1	23	52,2	62,4	2,3
2	Pa-S_056	oriC T-C_mut_1	GAAGCCCGGCGAATTCGGTGTTC	1	23	56,5	64,2	14,15
3	Pa-S_057	oprL T-C_wt	GGTGGTGGAGGGTGTTCGCCCGG	1	23	69,6	69,6	4,5
4	Pa-S_056	oprL T-C_mut_1	GGTGGTGGAGGGGCGTTTCGCCCGG	1	23	73,9	71,3	16,17
5	Pa-S_059	flhC A-T_wt	CAAGATCGCGCGGCGAGCGGTCAAC	1	22	63,6	65,8	6,7
6	Pa-S_059	flhC A-T_mut_1	CAAGATCGCGCGGTTCGCCGTCAAC	1	22	63,6	65,8	18,19
7	Pa-S_061	alkB2 G-A_wt	TGCTGCTGGCGCGCGGTGTGTAT	1	23	65,2	67,8	8,9
8	Pa-S_062	alkB2 G-A_mut_1	TGCTGCTGGCGCGGTGTGTAT	1	23	60,9	66,0	20,21
9	Pa-S_053	alkB2 A-G_wt	CGTGGCCCTGTTCGCCACCGCTCTGG	1	25	72,0	72,8	10,11
10	Pa-S_064	alkB2 A-G_mut_1	CTGGCCCTGTTCGCCACCGCTCTGG	1	24	75,0	73,0	22,23
11	Pa-S_065	ots A-G_wt	TGGAGCACTGGCGAGGAAATCCG	1	24	54,2	64,4	26,27
12	Pa-S_066	ots A-G_mut_1	CGAGCACTGGCGGAGAAATCCG	1	23	60,9	66,0	38,39
13	Pa-S_057	ots G-C_wt	CGGAAACTTCCTGCACATGATGTT	1	26	46,2	63,2	28,29
14	Pa-S_058	ots G-C_mut_1	CGGAAACTTCCTGCACATGATGTT	1	26	46,2	63,2	40,41
15	Pa-S_059	oprL T-C_wt	AGCTGACGACGACCGCTGACGAG	1	23	60,9	66,0	30,31
16	Pa-S_070	oprL T-C_mut_1	AGCTGACGACGACCGCTGACGAG	1	22	63,6	65,8	42,43
17	Pa-S_071	ampC_1 G-A_wt	ASGAGGACGGCCCGCGGTCAAGCC	1	25	76,0	74,5	32,33
18	Pa-S_072	ampC_1 G-A_mut_1	ASGAGGACGGCCCGCGGTCAAGCC	1	26	73,1	74,3	44,45
19	Pa-S_070	ampC_2 C-T_wt	GACAGGATGGCGCTCGACGACC	1	22	63,6	65,8	34,35
20	Pa-S_073	ampC_2 C-T_mut_1	GACAGGATGGCGCTCGACGACC	1	23	60,9	66,0	46,47
21	Pa-S_071	ampC_3 C-T_wt	AGCCCACTACCGCGCGGGCGAG	1	22	77,3	71,4	50,51
22	Pa-S_074	ampC_3 C-T_mut_1	AGCCCACTACCGCGCGGGCGAG	1	23	73,9	71,3	62,63
23	Pa-S_075	ampC_4 G-A_wt	CCCTTCGACCGCTCATGGAGCA	1	23	60,9	66,0	52,53
24	Pa-S_076	ampC_4 G-A_mut_1	CCCTTCGACCGCTCATGGAGCA	1	24	58,3	66,1	64,65
25	Pa-S_077	ampC_5 G-C_wt	TGGGCGAGCAAGTGTTCGCCCG	1	22	63,6	65,8	54,55

FIGURE 18B

26	Pa-S_070	ampC_5 G-	1	22	63,6	65,8	66,67
27	Pa-S_027	C_mut_1	1	24	58,3	66,1	56,57
28	Pa-S_076	ampC_6 T-C_wt	1	23	60,9	66,0	58,69
29	Pa-S_029	ampC_6 T-	1	22	68,2	67,7	58,59
30	Pa-S_030	C_mut_1	1	22	63,6	65,8	70,71
31	Pa-S_031	ampC_7 C-A_wt	2	24	58,3	66,1	74,75
32	Pa-S_032	ampC_7 C-	2	23	56,5	64,2	66,87
33	Pa-S_033	flilC b	3	22	68,2	67,7	76,77
34	Pa-S_034	flilC a	3	24	58,3	66,1	88,89
35	Pa-S_035	exoS-1	4	24	54,2	64,4	78,79
36	Pa-S_036	exoU	4	24	58,3	66,1	90,91
37	Pa-S_037	C-47-1	5	24	54,2	64,4	80,81
38	Pa-S_038	C-47-2	5	24	58,3	66,1	92,93
39	Pa-S_039	47D7-1	6	24	54,2	64,4	82,83
40	Pa-S_040	47D7-2	6	24	58,3	66,1	94,95
41	Pa-S_041	C-45	7	24	54,2	64,4	86,99
42	Pa-S_042	C-46	7	24	58,3	66,1	110,111
43	Pa-S_043	C-inselspez-4	8	24	58,3	66,1	122,123
44	Pa-S_044	C-inselspez-5	9	24	54,2	64,4	100,101
45	Pa-S_045	C-spezifisch-1	9	24	54,2	64,4	112,113
46	Pa-S_046	pKL-3	9	25	52,0	64,6	124,125
47	Pa-S_047	pKL-7	10	24	58,3	66,1	102,103
48	Pa-S_048	PAGI-1-1	10	24	58,3	66,1	114,115
49	Pa-S_049	PAGI-1-8	11	24	58,3	66,1	104,105
50	Pa-S_050	SG17M-1	11	24	54,2	64,4	116,117
51	Pa-S_051	SG17M-4	12	24	58,3	66,1	106,107
52	Pa-S_052	fla-insel-1	13	24	58,3	66,1	118,119
53	Pa-S_053	TB-C47-1	13	24	54,2	64,4	126,127
54	Pa-S_054	TB-C47-2	13	24	58,3	66,1	128,129
55	Pa-S_055	TB-C47-3	13	24	58,3	66,1	128,129

FIGURE 18C

55	Pa-S_052	TB-C47-4	CGCTGCACATACAGGTCGGTTCTC	13	24	54,2	64,4	130,131
56	Biotin + Cy3-marker							1,12,97,121,132
57	Pa-S_081	oriC T-C_wt_1	AGCCCAGCAATTGCGTGTCTCTCCG	1	25	65,6	56	
58	Pa-S_082	oriC T-C_mut_2	AGCCCAGCAACTGCCGTGTTCTCTCC	1	24	65,1	58	
59	Pa-S_083	alkB2 G-A_wt_2	GCTGCTGGCGCGGTGTGC		19	67,4	79	8,9
60	Pa-S_084	alkB2 G-A_mut_2	TGCTGTGGCAGCGGTGTGCT		21	67,3	67	20,21
61	Pa-S_085	oprI T-C_wt_2	CAGAAAGCTCAGCAGACTGCTGACGAG		27	64,6	56	
62	Pa-S_086	oprI T-C_mut_2	GAAAGCTCAGCAGACCGCTGACGAG		25	64,9	60	
63	Pa-S_087	ampC_1 G-A_wt_2	ACGGCCGCCGGGTGACGCC		19	70,2	84	
	ampC_1 G-							
64	Pa-S_088	A_mut_2	ACGGCCGCCAGGTGACGCCG		20	69,9	80	
65	Pa-S_089	ampC_3 C-T_wt_1	GCCGACCTACGCCGCCGGC		19	68,4	84	
	ampC_3 C-							
66	Pa-S_090	T_mut_2	AGCCGACCTATGCCGCCGGGCA		21	68,4	71	
67	Pa-S_091	ampC_4 G-A_wt_2	GTTCCGAACGGCTCATGGAGCAGCA		24	65	58	
	ampC_4 G-							
68	Pa-S_092	A_mut_2	GTTCCGAACGACTCATGGAGCAGCAAG		26	63,5	54	
69	Pa-S_093	exoS-1_1	CAGCCCAGTCAGGACGCCGA		20	64,9	70	
70	Pa-S_094	exoU_1	AGTGACGTGCCGTTTCAGCAGTCCC		24	64,8	58	
71	Pa-S_095	47D7-1_1	GTGTCACGGCCCCATGTCTAGCAGC		24	65	63	
72	Pa-S_096	C-46_1	CGAAGTCTGAGGTGTGGACCCGC		23	64,5	65	
73	Pa-S_097	Fla-Insel-2_orfA	CGCTGGAGGGTATGTTCCGCAAGG		24	64,8	63	
74	Pa-S_098	Fla-Insel-2_orfC	CGTACTCAGCTTCTCCACCCAGCG		24	64,3	63	
75	Pa-S_099	Fla-Insel-2_orfI	CCTGGACCTCTCCAAGGTTGCGCT		24	65	63	
76	Pa-S_100	Fla-Insel-2_orfJ	GCCATTCCGACGACCAAAACAAGGC		24	64,2	58	

group "mother"

REPLACEMENT SHEET

Atty Docket: 15111.0087

FIGURE 19A

seq no	name	5'-3'-sequence	group	length	GC-content [%]	Tm [°C]	spot-ID's
1	Pa-S_001	oriC T-C_wt					
2	Pa-S_002	oriC T-C_mut_1					
37	Pa-S_061	oriC T-C_wt_1					
55	Pa-S_062	oriC T-C_mut_2					
3	Pa-S_067	opd T-C_wt_1					
4	Pa-S_068	opd T-C_mut_1					
5	Pa-S_069	HKa A-T_wt_1					
6	Pa-S_070	HKa A-T_mut_1					
59	Pa-S_083	alkB2 G-A_wt_2					
60	Pa-S_084	alkB2 G-A_mut_2					
9	Pa-S_093	alkB2 A-G_wt_1					
10	Pa-S_094	alkB2 A-G_mut_1					
11	Pa-S_095	cts A-G_wt_1					
12	Pa-S_096	cts A-G_mut_1					
13	Pa-S_097	cts G-C_wt_1					
14	Pa-S_098	cts G-C_mut_1					
15	Pa-S_099	opd T-C_wt_1					
16	Pa-S_070	opd T-C_mut_1					
61	Pa-S_095	opd T-C_wt_2					
62	Pa-S_086	opd T-C_mut_2					
63	Pa-S_097	ampC_1 G-A_wt_2					
64	Pa-S_098	ampC_1 G-A_mut_2					
19	Pa-S_019	ampC_2 C-T_wt					
20	Pa-S_073	ampC_2 C-T_mut_1					
21	Pa-S_021	ampC_3 C-T_wt					
22	Pa-S_074	ampC_3 C-T_mut_1					

FIGURE 19B

65	Pa-S_089	ampC_3 C-T_wt_1	GCCGACCTACGGCGCGGGG	1	19	68,4	84	36,48
66	Pa-S_090	ampC_3 C-T_mut_2	ATCCGACCTATGCGCGCGGGCA	1	21	68,4	71	60,72
67	Pa-S_091	ampC_4 G-A_wt_2	GTTGGAACGGCTCATGGAGCAGCA	1	24	65	58	52,53
68	Pa-S_092	ampC_4 G-A_mut_2	GTTGGAACGACTCATGGAGCAGCAAG	1	26	63,5	54	64,65
69	Pa-S_077	ampC_5 G-C_wt_1	TGGAGCAGCAGTAGTGTTCGCGGC	1	22	63,6	65,8	54,55
70	Pa-S_078	ampC_5 G-C_mut_1	TGGAGCAGCAGCACTGTTCGCGGC	1	22	63,6	65,8	66,67
71	Pa-S_027	ampC_6 T-C_wt	GAACAAGACCGGTTCCACCAACGG	1	24	58,3	66,1	55,57
72	Pa-S_079	ampC_6 T-C_mut_1	AACAGACACCGGCTCCACCAACGG	1	23	60,9	66,0	68,69
73	Pa-S_029	ampC_7 C-A_wt	GCGACCTGGCGCTGGTGATCCT	1	22	68,2	67,7	58,59
74	Pa-S_080	ampC_7 C-A_mut_1	GCGACCTGGGACTGGTGATCCT	1	22	63,6	65,8	70,71
75	Pa-S_031	fliC b	GCCGACCACTGACTCCACTCG	2	24	58,3	66,1	74,75
76	Pa-S_082	fliC a	GCGGCTGACCGCACTACTTCA	2	23	56,5	64,2	88,87
77	Pa-S_083	exoS-1_1	GAGGCGAGTCAAGGCGCGGAA	3	20	64,9	70	76,77
78	Pa-S_084	exoS	GCGCAGTTCAGAACGGAGTCAC	3	24	58,3	66,1	88,89
79	Pa-S_084	exoS_1	AGTACGTCGGTTCAGGCGTCCC	3	24	64,8	58	84,86
80	Pa-S_038	C-47-1	GCGCGATCTTCTGCACTTCATCGG	4	24	54,2	64,4	78,79
81	Pa-S_035	47D7-1_1	GTGTACCGGCCCATGTCTAGCAGG	5	24	65,2	63	80,81
82	Pa-S_041	47D7-2	GTGAGCATGGATCGGCAGTCGTT	5	24	58,3	66,1	92,93
83	Pa-S_054	C-45	CGACCGATTCGGACCGGCTTTGA	6	24	54,2	64,4	82,83
84	Pa-S_055	C-46	AATAGGACCGGCAGAACGGGCATT	6	24	58,3	66,1	94,95
85	Pa-S_056	C-46_1	CGAAGTCGAGGTGTGGACCCGC	6	23	64,5	65	108,120
86	Pa-S_035	C-Inselspez-4	GCGCCTTCTCCTCTTTCAGATGT	7	24	54,2	64,4	98,99
87	Pa-S_036	C-Inselspez-5	CAGTATGTTACCGACACGAGCGC	7	24	58,3	66,1	110,111
88	Pa-S_037	C-spezifisch-1	GCATCATTCGCGCTCAGATCTGGT	8	24	58,3	66,1	122,123
89	Pa-S_044	pKL-3	TCTGAATCGGGCTATCACCTGCA	9	24	54,2	64,4	100,101
90	Pa-S_046	pKL-11	AGTCATGGGACTGATATACGGGACT	9	25	52,0	64,6	124,125
91	Pa-S_042	PAGI-1-1	TTCTCGGTGTCGAGGATTCGCG	10	24	58,3	66,1	102,103
92	Pa-S_043	PAGI-1-8	TGGTAGCTCTCGACGCTACTCGCTG	10	24	58,3	66,1	114,115

FIGURE 19C

49	Pa-S_047	SG17M-1	CCCGTTGCTCATACCCGGTCCCTG	11	24	58,3	66,1	104,105
50	Pa-S_048	SG17M-4	AGGGCATTTCTCAGGTGGACTCAGG	11	24	54,2	64,4	116,117
51	Pa-S_053	fla-insel-1	ACCTGTGTGGCTGGAGGGTATGTT	12	24	58,3	66,1	108,107
54	Pa-S_051	TB-C47-3	TCCATCAGGCGAGGATACAGGGTG	13	24	58,3	66,1	128,129
55	Pa-S_052	TB-C47-4	CGCAGCATACACAGGTCCGTTCTC	13	24	54,2	64,4	130,131
73	Pa-S_037	Fla-Insel-2_orfA	CGCTGAGGGGTATGTTCCGGCAGG	14	24	64,8	63	90,91
74	Pa-S_038	Fla-Insel-2_orfC	CGTACTCAGCTTCTCCACCCAGCG	14	24	64,3	63	112,113
75	Pa-S_039	Fla-Insel-2_orfI	CCTGGACCTCTCCAGGTTCCGCT	14	24	65	63	118,119
76	Pa-S_100	Fla-Insel-2_orfJ	GCCATTCCGACGACCCAAACAGGC	14	24	64,2	58	126,127
56	Bio10 + O ₂ -marker							1,12,97,121,132

group "mother"

FIGURE 20

Chip: MHH_P_aer_array2 (12x11 array with spot distance of 19.00 mm)

56	43	43	46	46	76	76	54	54	55	55	56
	42	42	74	74	48	48	50	50	75	75	72
56	41	41	44	44	47	47	49	49	51	51	72
62	32	32	34	34	73	73	38	38	40	40	70
61	31	31	69	69	35	35	71	71	39	39	70
61	22	22	68	68	26	26	28	28	30	30	66
58	21	21	67	67	25	25	27	27	29	29	66
58	12	12	14	14	16	16	64	64	20	20	65
57	11	11	13	13	15	15	63	63	19	19	65
57	2	2	4	4	6	6	60	60	10	10	62
56	1	1	3	3	5	5	59	59	9	9	56

FIGURE 21

Chip occupancy

marker spot	C-spezifisch-1	pKL-11	Fla-Insel-2_orfJ	TB-C47-3	TB-C47-4	marker spot
mut_2 opr1 T-C wt_2 opr1 T-C wt_2	C-Insel-spezifisch-5 C-Insel-spezifisch-4	Fla-Insel-2_orfC	PAGI-1-8	SG17M-4	Fla-Insel-2_orfI	C-46_1
		pKL-3	PAGI-1-1	SG17M-1	fla-Insel-1	C-46_1
mut_2 opr1 T-C wt_2 opr1 T-C wt_2	flic A flic B	exoU	Fla-Insel-2_orfA	47D7-2	C-46	exoU_1
		exoS-1_1	C-47-1	47D7-1_1	C-45	exoU_1
mut_2 oriC T-C mut_2 oriC T-C wt_1 oriC T-C wt_1	mut_1 ampC_3 C-T wt mut_1 citS A-G wt_1 mut_1 oriC T-C wt_1	mut_2 ampC_4 G-A wt_2	mut_1 ampC_5 G-C wt_1	mut_1 ampC_6 T-C wt	mut_1 ampC_7 C-A wt	mut_2 ampC_3 C-T mut_2 ampC_3 C-T wt_1 ampC_3 C-T wt_1
mut_2 opr1 T-C wt_2 opr1 T-C wt_2	mut_1 oriC T-C wt	mut_1 opr1 T-C wt_1	mut_1 opr1 T-C wt_1	mut_2 ampC_1 G-A wt_2	mut_1 ampC_2 C-T wt	opr1 T-C mut_2 alkB2 A-G wt_1
						marker spot